RESPONSE TO RESTRICTION REQUIREMENT DATED 07/11/06

Sir:

This is in response to the Non-Final Office Action that was mailed on July 11, 2006. The following amendments and remarks are respectfully submitted.

Amendments to the claims begin on page 3 of this Response.

Remarks begin on page 13 of this Amendment.

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

The invention claimed is:

1. (Original) A method in a computing environment for documenting mutations, the method comprising:

receiving mutation information;

disassembling the mutation information into discrete elements; and

storing said discrete elements such that the mutation may be presented using both user-preferred and published standards.

2. (Withdrawn) The method of claim 1, wherein the mutation information is for one of a substitution, inversion, insertion, deletion, translocation, complex rearrangement and combinations thereof.

3. (Withdrawn) The method of claim 1, wherein the discrete elements include a mutation identification value.

4. (Withdrawn) The method of claim 1, wherein the discrete elements include a patient identification value.

5. (Withdrawn) The method of claim 1, wherein the discrete elements include the mutation type.

6. (Withdrawn) The method of claim 1, wherein the discrete elements include a reference sequence identification value.

7. (Withdrawn) The method of claim 1, wherein the discrete elements include a starting point value within the reference sequence.

8. (Withdrawn) The method of claim 1, wherein the discrete elements include an ending point within the reference sequence.

9. (Withdrawn) The method of claim 1, wherein the discrete elements include the length of an insertion

10. (Withdrawn) The method of claim 1, wherein the discrete elements include the native value of sequenced genetic information

11. (Withdrawn) The method of claim 1, wherein the discrete elements include an observed value of the mutation.

12. (Original) The method of claim 10, wherein the native value of sequenced genetic information is one or more nucleotides or amino acids.

13. (Original) The method of claim 11, wherein the observed value of sequenced genetic information is one or more nucleotides or amino acids.

14. (Original) The method of claim 1, wherein the user-preferred standards are user defined.

15. (Original) The method of claim 1, wherein the published standards are the recommended standards published the Human Genome Association.

16. (Withdrawn) The method of claim 1, wherein the published standards are the standards adopted by the genetics community.

17. (Original) The method of claim 1, further comprising:

providing a list of known mutations for particular sequenced genetic information.

18. (Original) The method of claim 17, wherein the sequenced genetic information is one of a gene, a protein, sequenced DNA other than a gene and sequenced RNA.

19. (Original) The method of claim 18, further comprising:

receiving a selection of a mutation from the list of known mutations.

20. (Original) The method of claim 17, further comprising:

receiving a request for the reference sequence for the sequenced genetic information.

21. (Original) The method of claim 20, further comprising:

providing the reference sequence for the sequenced genetic information.

22. (Original) The method of claim 21, further comprising:

providing data entry fields for the entry of mutation information.

23. (Original) The method of claim 22, wherein the data entry fields include one or more of the position of the mutation and the value of the mutation.

24. (Original) The method of claim 23, further comprising:

receiving mutation type.

25. (Original) The method of claim 24, further comprising:

receiving regarding the observed mutation.

26. (Withdrawn) The method of claim 1, wherein the mutation information is for one of humans, animals, vertebrates, invertebrates, plants, viruses, bacteria, fungi, prokaryotes, eukaryotes, and protista

27. (Withdrawn) The method of claim 26, wherein the mutation information is for a particular patient.

28. (Original) The method of claim 27, further comprising:

identifying the patient in connection with the mutation information and the discrete values.

29. (Original) A method in a computing environment for presenting mutations, the method comprising:

obtaining the discrete elements for mutation information;

obtaining a standard for presenting the mutation information; and

assembling the mutation information utilizing the discrete elements and the standard of presentation.

30. (Original) The method of claim 29, wherein the standard is one of a user-preferred standard and a published standard.

31. (Original) The method of claim 30, wherein the user-preferred standard is user defined.

32. (Original) The method of claim 30, wherein the published standard is published by the Human Genome Association.

33. (Withdrawn) The method of claim 30, wherein the published standards are the standards adopted by the genetics community.

34. (Original) A computer system for documenting mutations, the system comprising:

a receiving module for receiving mutation information;

a disassembling module for disassembling the mutation information into discrete elements; and

a storage module stores said discrete elements such that the mutation may be presented using both user-preferred and published standards.

35. (Withdrawn) The system of claim 34, wherein the mutation information is for one of a substitution, inversion, insertion, deletion, translocation, complex rearrangement and combinations thereof.

36. (Withdrawn) The system of claim 34, wherein the discrete elements include one or more of a mutation identification value, patient identification value, mutation type, reference sequence identification value, starting point value within the reference sequence, ending point within the reference sequence, length of an insertion, native value of sequenced genetic information, observed value of the mutation.

37. (Original) The system of claim 34, wherein the user-preferred standards are user defined.

38. (Original) The system of claim 34, wherein the published standards are the recommended standards published the Human Genome Association.

39. (Withdrawn) The system of claim 34, wherein the published standards are the standards adopted by the genetics community.

40. (Original) The system of claim 34, further comprising:

a providing module for providing a list of known mutations for particular sequenced genetic information.

41. (Original) The system of claim 40, wherein the sequenced genetic information is a gene.

42. (Original) The system of claim 40, further comprising:

a second receiving module for receiving a selection of a mutation from the list of known mutations.

43. (Original) The system of claim 40, further comprising:

a third receiving module receiving a request for the reference sequence for the sequenced genetic information.

44. (Original) The system of claim 43, further comprising:

a second providing component for providing the reference sequence for the sequenced genetic information.

45. (Original) The system of claim 44, further comprising:

a third providing component for providing data entry fields for the entry of mutation information.

46. (Original) A computer system for presenting mutations, the method comprising:

an obtaining component for obtaining the discrete elements for mutation information;

a second obtaining component for obtaining a standard for presenting the mutation information; and

an assembling component for assembling the mutation information utilizing the discrete elements and the standard of presentation.

47. (Original) The system of claim 46, wherein the standard is one of a user-preferred standard and a published standard.

48. (Original) The system of claim 47, wherein the user-preferred standard is user defined.

49. (Original) The system of claim 47, wherein the published standard is published by the Human Genome Association.

50. (Withdrawn) The system of claim 47, wherein the published standards are the standards adopted by the genetics community.

51. (Original) A computer-readable medium having computer-executable instructions for performing a method, the method comprising:

receiving mutation information;

disassembling the mutation information into discrete elements; and

storing said discrete elements such that the mutation may be presented using both user-preferred and published standards.

52. (Original) A computer-readable medium having computer-executable instructions for performing a method, the method comprising:

obtaining discrete elements for a mutation;

obtaining a standard for presenting the mutation information; and

assembling the mutation information utilizing the discrete elements and the standard of presentation.

53. (Original) A computer system for documenting mutations, the method comprising:

means for receiving mutation information;

means for disassembling the mutation information into discrete elements; and

means for storing said discrete elements such that the mutation may be presented using both user-preferred and published standards.

54. (Original) A computer system for presenting mutations, the method comprising:

means for obtaining the discrete elements for mutation information;

means for obtaining a standard for presenting the mutation information; and means for assembling the mutation information utilizing the discrete elements and the standard of presentation.

55. (Withdrawn) A method for receiving mutation information from a user, comprising:

displaying a reference sequence for sequenced genetic information;

providing one or more data entry fields for entry of mutation information; and

receiving information regarding the observed mutation such that the mutation may be presented using both user-preferred and published standards.

56. (Withdrawn) The method of claim 55, wherein the mutation information includes mutation type.

57. (Withdrawn) The method of claim 55, wherein the mutation information includes the observed mutation.

58. (Withdrawn) The method of claim 55, wherein the mutation information includes edits relative to a reference sequence.

59. (Withdrawn) A method of displaying mutation information in one or more data fields, the method comprising:

providing a reference sequence for sequenced genetic information;

receiving edits relative to the reference sequence for an observed mutation; and

displaying the edits in one or more data fields.

60. (Withdrawn) The method of claim 59, wherein the data fields include a mutation type field.

61. (Withdrawn) The method of claim 59, wherein the data fields include a field reflecting the starting point of the mutation within the reference sequence.

62. (Withdrawn) The method of claim 59, wherein the data fields include a field reflecting the ending point of the mutation within the reference sequence the observed mutation end.

63. (Withdrawn) The method of claim 59, wherein the data fields include a field for the observed value of the mutation.

64. (Withdrawn) The method of claim 59, wherein the data fields include a field for the position of the mutation within the reference sequence.